histopathological types. On immunostaining expression pattern of CK in large cell carcinoma was similar to that of adenocarcinoma.

Conclusion: The investigations of CK expression give us additional information concerning histopathological differentiation of primary lung cancer. Though more investigations are needed, there is a strong possibility that classification based upon proteomic analysis, as well as morphological features, may reflect the biological characteristics of tumor cells.

P2-060 **BSTB: Others Posters, Tue, Sept 4**

Altered iron metabolism, inflammation, transferrin receptors and ferritin expression in lung cancer

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Introduction: Alterations in whole-body iron metabolism are known to occur in patients with cancer. Iron could participate in carcinogenesis and overabundance of iron is associated with increased risk of neoplasia at the site of metal deposition.

Aim: The relationship between the iron status and survival of lung cancer patients and the expression of transferrin receptors 1 (TfR1) and ferritin in tumor tissue, tumor stroma and normal lung were studied.

Patients and Methods: These findings were correlated with tumor type and clinical outcome in 111 male patients. Iron metabolism and inflammation parameters were determined by automated laboratory measurements at the time of diagnosis. TfR1 and ferritin expression were determined by immuno-histochemical methods on cancer tissue, tumor stroma and on the surrounding normal lung tissue.

Results: More than fifty percentages of patients survived less than 12 months. At the time of diagnosis approximately a half of the patients had mild anemia of chronic disease and significantly elevated serum ferritin. Nonspecific laboratory markers of inflammation were present. Tumor tissue expressed much more TfR1 and ferritin than the tumor stroma and normal lung tissue. The expression of TfR1 and the ferritin content in tumor tissue depended on the carcinoma type. TfR1 and the ferritin content in tumor tissue did not show correlation with systemic parameters of most of iron metabolism parameters. Strong ferritin expression in tumor tissue correlates only with lower transferin saturation.

Conclusion: Higher expression of ferritin in tumor tissue is not the results of higher body iron accumulation. Elevated serum ferritin in lung cancer patients is results of inflammation and oxidative stress rather than body iron overload.

P2-061 **BSTB: Others Posters, Tue, Sept 4**

ProGRP and NSE for follow-up of small cell lung cancer patients with limited disease

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Introduction: For some years, NSE has been known as a marker of choice for small cell lung cancer. However, its diagnostic sensitivity and specificity are not completly satisfactory, due to relatively high false negative rate in SCLC patients with limited disease and false positive rate in patients with non-malignant lung disease and non-small cell lung cancer. Recently, the usefulness of pro-gastrin-releasing peptide (ProGRP) as a tumor marker for SCLC has been investigated. Although the diagnostic sensitivity and specificity of ProGRP was found to be higher than serum NSE, only small number of data concern its utility in disease therapy monitoring and its value in prediction of response to treatment. The aim of the study was the evalutation of ProGRP and NSE levels at the time of diagnosis and during chemo- and radiotherapy of SCLC patients with limited disease in respect to their prognosis.

Material and Methods: Studies of NSE and ProGRP were performed in a group of 52 SCLC-LD. Patients with SCLC with limited disease were treated simultaneously with chemo and radiotherapy. All of them also received prophylactic cranial irradiation between fourth and fifth course of chemotherapy. The increment ratio of tumor markers was calculated as serum concentration divided by the cut off, for assessment of prognostic value of these markers.

Results: ROC curve analysis confirmed that ProGRP was a better than NSE tumor marker for diagnostics of SCLC-LD patients (Area under curves ROC: 0.935 vs. 0.789, p = 0.000).

There were observed significant differences in the frequency of elevated NSE and ProGRP levels before each course of chemotherapy and 3 months after its finishing, respectively:1st 57.6% vs. 78.8%, 2nd 5.8% vs. 67.3%, 3th 0% vs. 36.5%, 4th 1.9% vs. 21.2%, in restaging 6.7% vs. 15.7%. Changes in NSE levels during therapy were more intensive than for ProGRP what was reflected in tumor markers half-life (NSE: 4.6 - 11 days; ProGRP: 19-28 days) as well as in the frequency of increment of tumor markers ratio values. Patients with tumor marker levels 2 times exceeding NSE cut off and 12.5-times ProGRP cut off before treatment, and those with NSE and ProGRP having these ratio values higher than 0.4 and 0.65 during restaging 3 months after finishing therapy has shown worse prognosis.

Multivariate analysis confirmed that independent prognostic factors in SCLC with limited disease were: NSE level exceeding 2-times cut off value before treatment as well as NSE threshold 0.4 cut off and 0.65 ProGRP cut off value 3 months after therapy.

Conclusions:

1 Changes of ProGRP during combined therapy of SCLC-LD seem to be more adequate to actual clinical status of patients than NSE
2. NSE before treatment is a better than ProGRP prognostic factor in SCLC-LD patients however after finishing therapy both markers have similar predictive value

P2-062 **BSTB: Others Posters, Tue, Sept 4**

Optimizing the yield of circulating DNA from plasma and serum

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Background: Low levels of circulating cell-free DNA are present in normal individuals. In cancer patients, much higher levels of circulating DNA are found. Importantly, circulating DNA in lung cancer patients demonstrates genetic alterations typical of the tumour, leading to interest in plasma and serum DNA for early clinical diagnosis, prognosis and disease monitoring. There is considerable variation among studies in the reported levels of circulating DNA and its characteristics, which may be attributable to differences in selection of the patient and control groups, and the methods used for DNA extraction and estimation of circulating DNA concentrations. Here, we compare the efficiency of different methods for extracting low-level circulating DNA from blood samples.